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WIN2 20818 WOUND INDUCIBLE 0

KNOX HOMEODOMAIN 20699

CHLOROPLAST ATPASE 23416 I

RNA BINDING 30848 I

UNKNOWN 29957 0

UNKNOWN 25358 0

CYCLIN Os49462 20325

ZINC FINGER POZ DOMAIN 29942 0

HEAVY MEROMYOSIN 23484 0

PUTATIVE Mg TRANSPORTER 29970 0

CORA-LIKE Mg TRANSPORTER 25381 0

UNKNOWN 29075 0

SOLUBLE STARCH SYNTHASE 19701 0

UNKNOWN 29950 0

CALRETICULIN 20544 TRANSMEMBRANE 0

OsHD1 HISTONE DEACETYLASE 24059 0

DEHYDRIN 20554 0

SENESCENCE ASSOCIATED 20462 TRANSMEMBRANE

MYOSIN VIII 23878 0

GAMMA HYDROXY-BUTYRATE DEHYDROGENASE 29037 I

LOW TEMPERATURE INDUCED 22883 TRANSMEMBRANE I

CALLOSE SYNTHASE 23226 0

COPROPORPHYRINOGEN OXIDASE 23485 0

PUTATIVE MYOSIN HEAVY CHAIN 23297 I

PUTATIVE MYOSIN HEAVY CHAIN 29882 I

PUTATIVE MYOSIN HEAVY CHAIN 29966 0

NUCLEAR MATRIX CONSTITUENT 29956 0

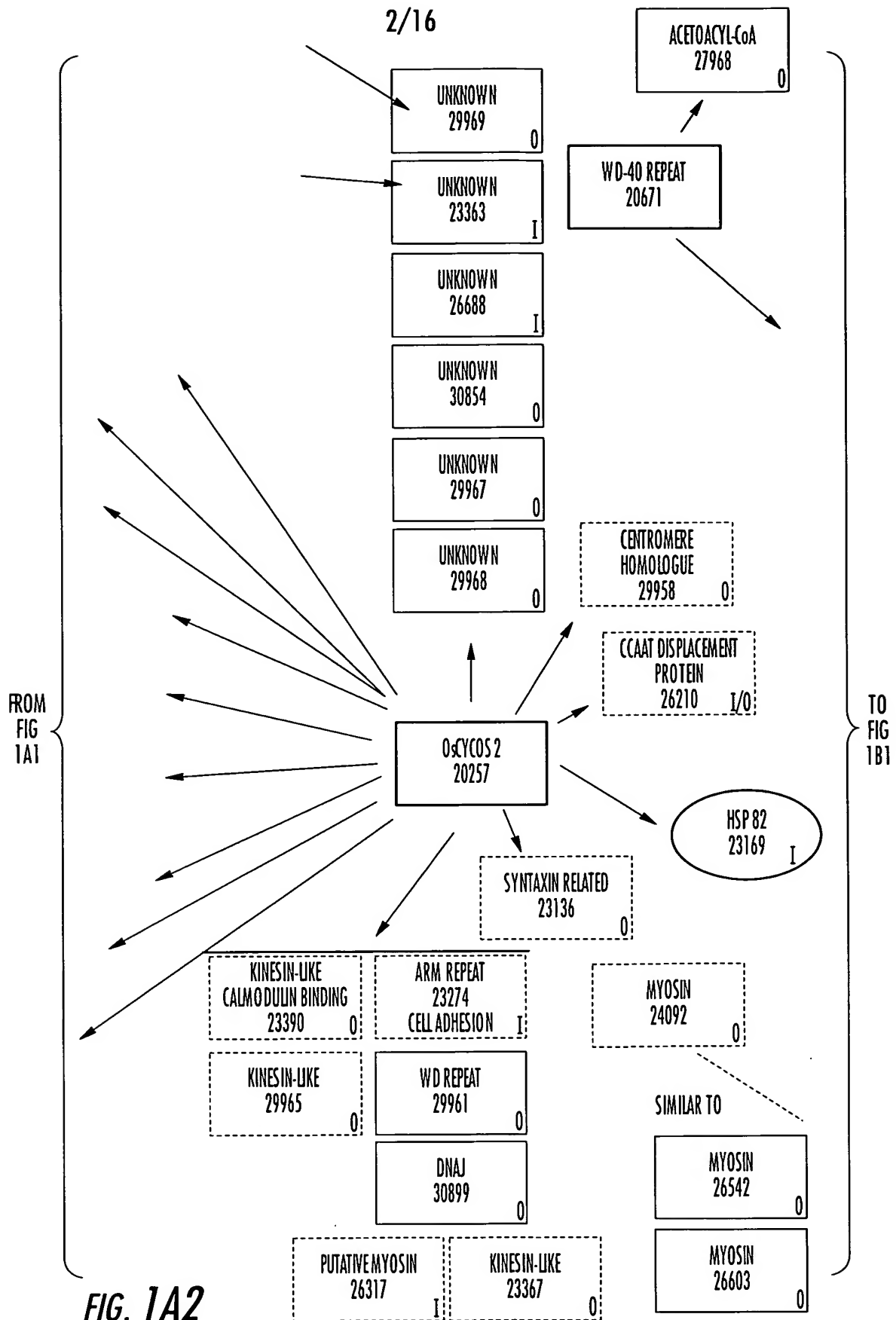
PUTATIVE MYOSIN HEAVY CHAIN 20815 0

FIG. 1A1

TO FIG 1A2

CELL CYCLE

TO FIG 1A3



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FROM FIG 1A2

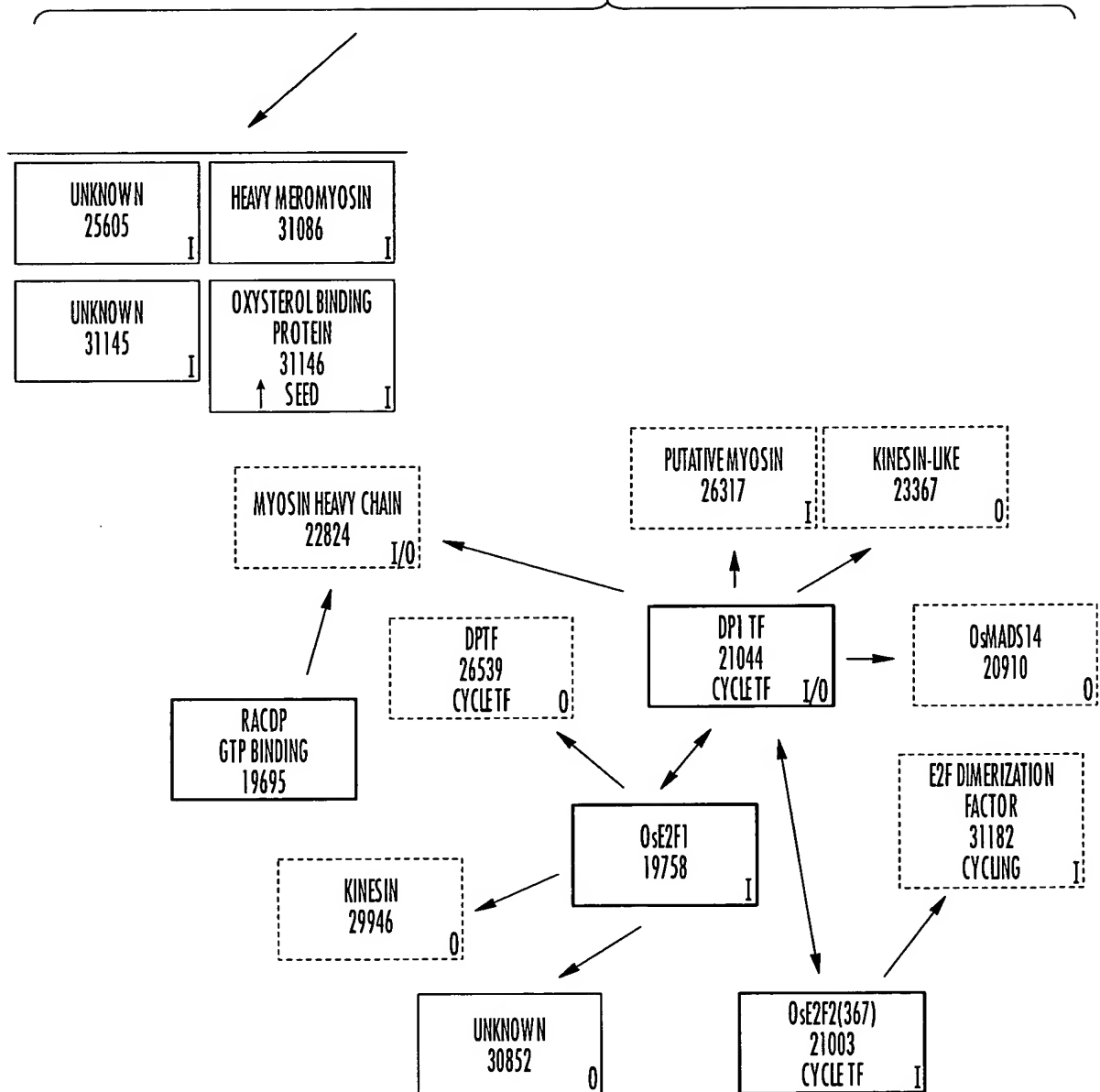
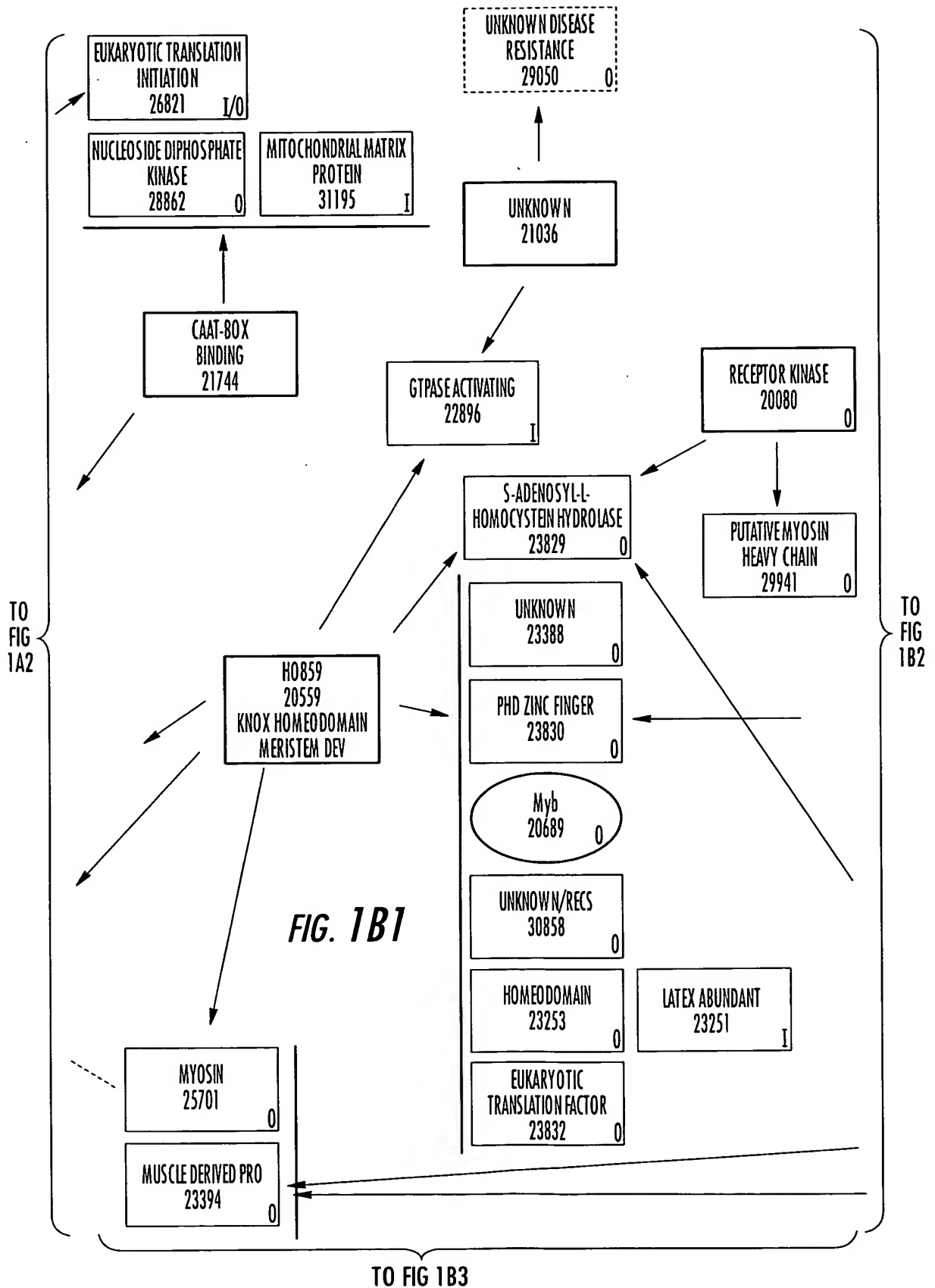


FIG. 1A3

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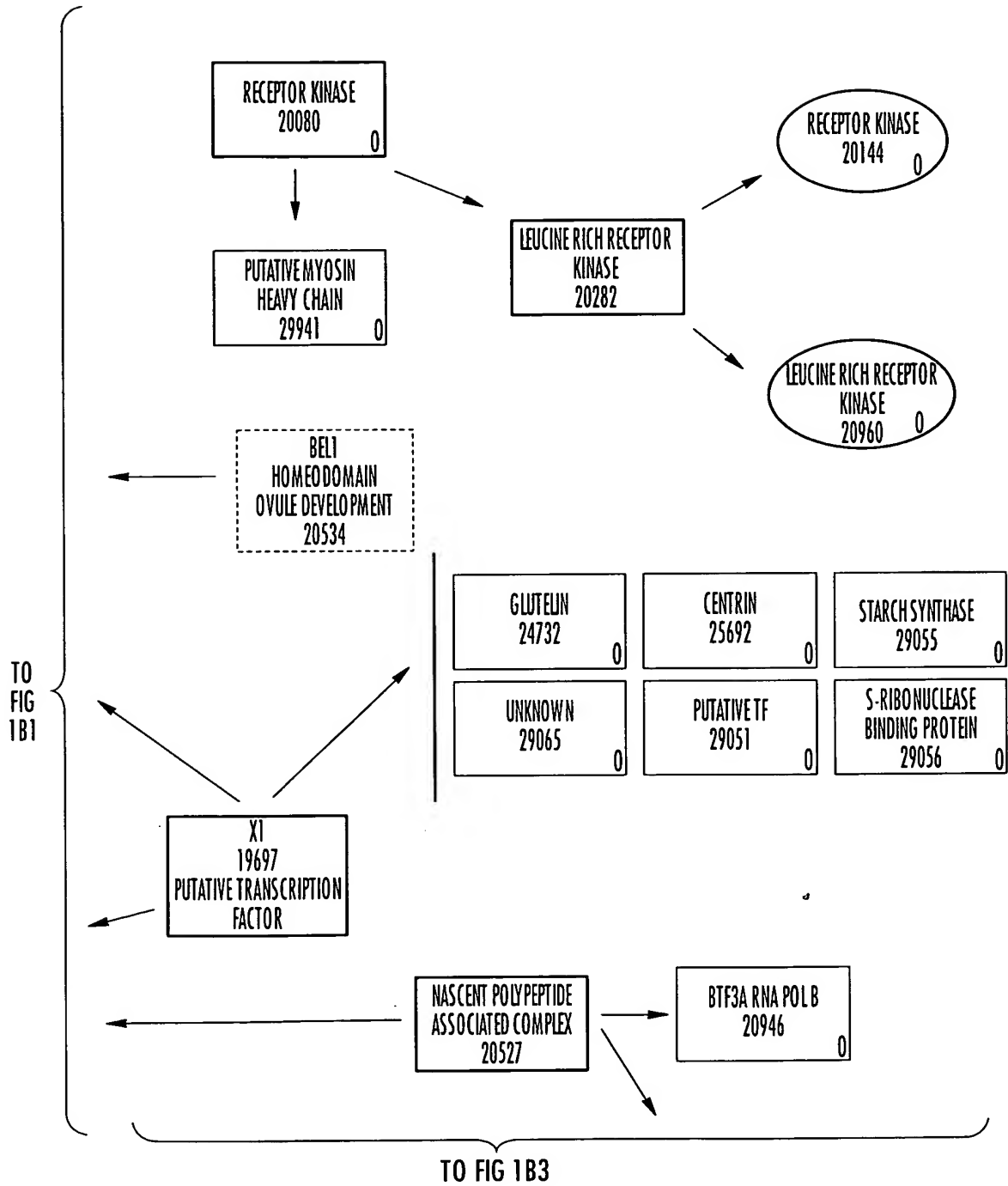


FIG. 1B2

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TO FIG 1B1 AND 1B2

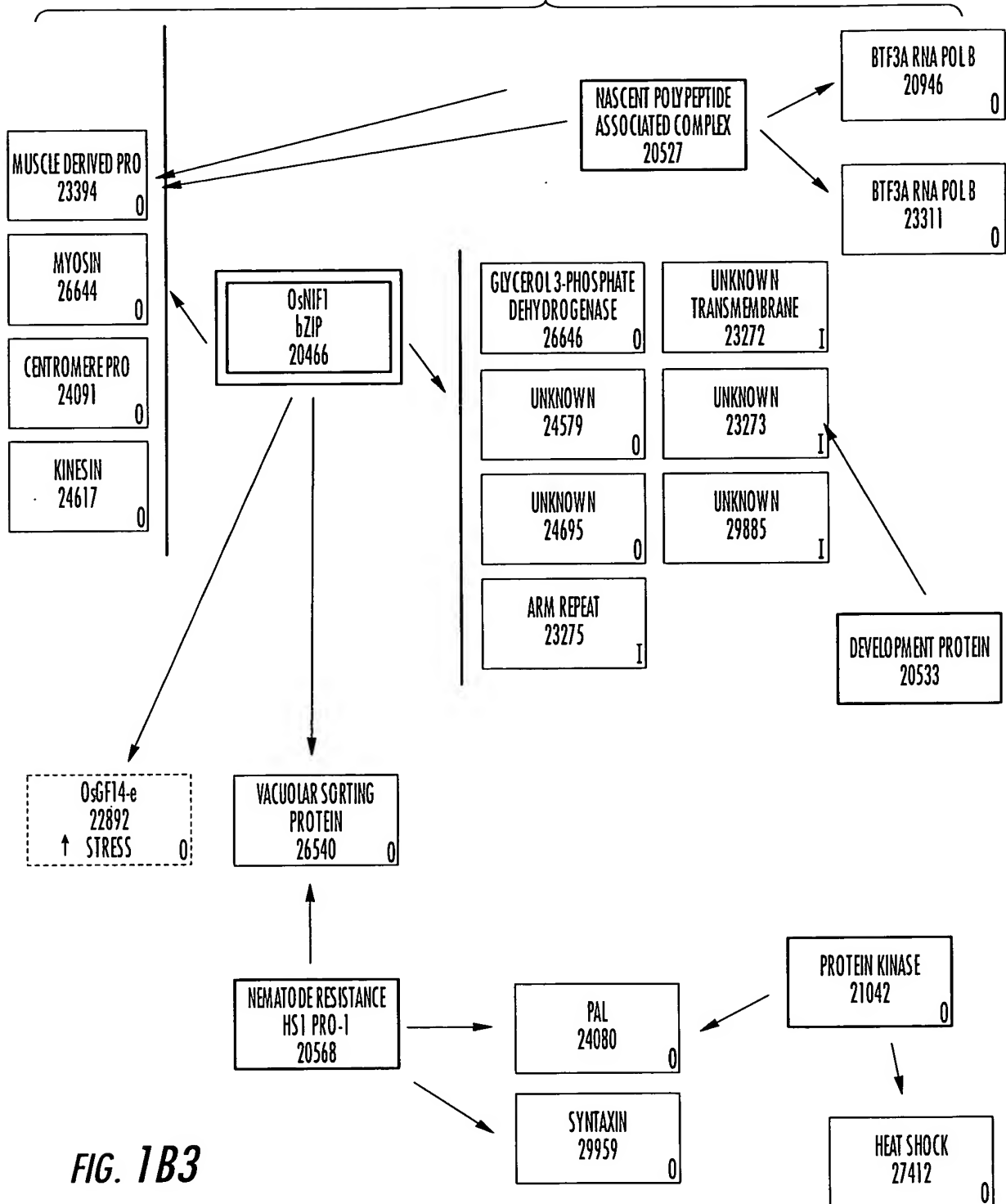
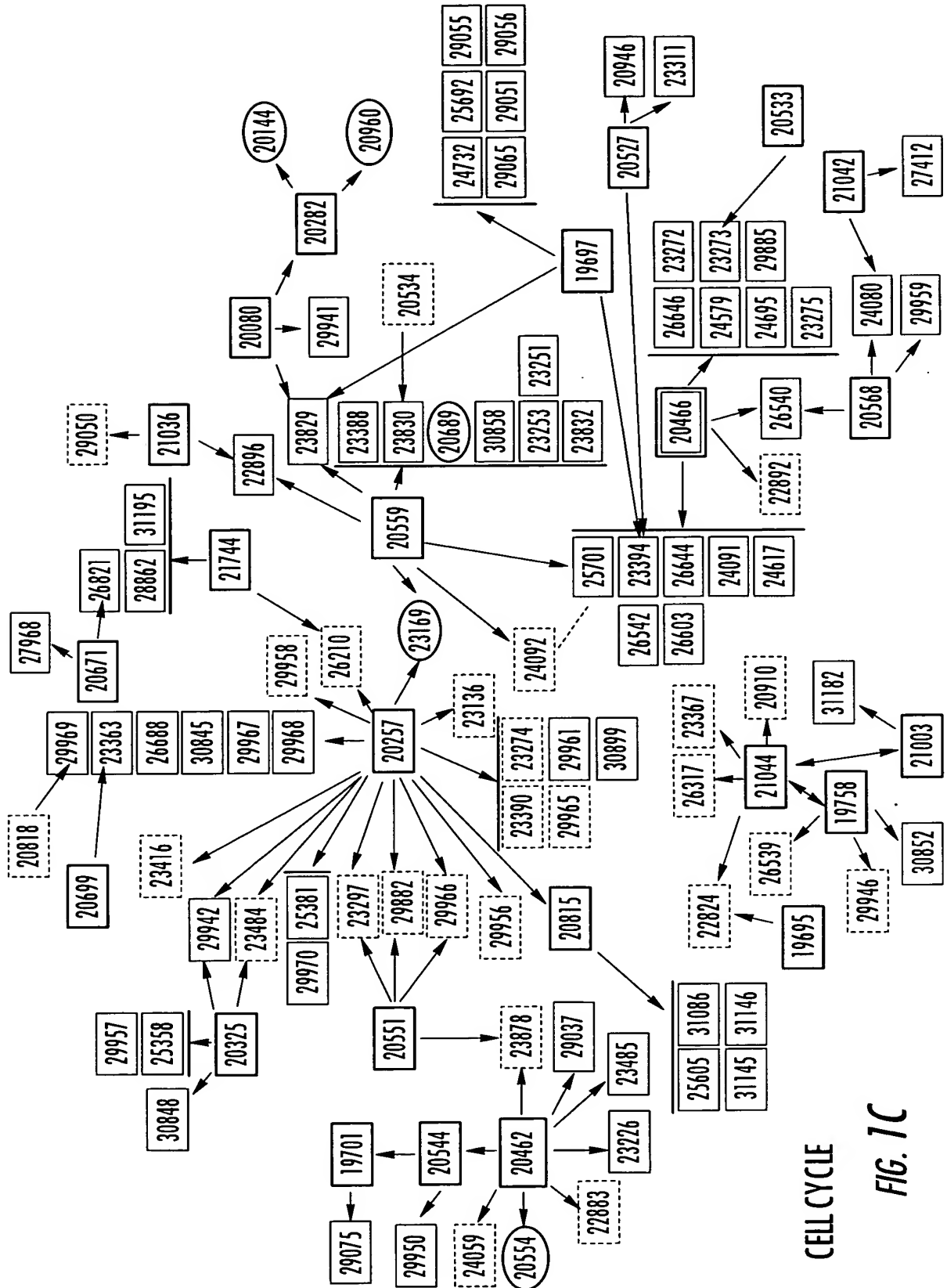


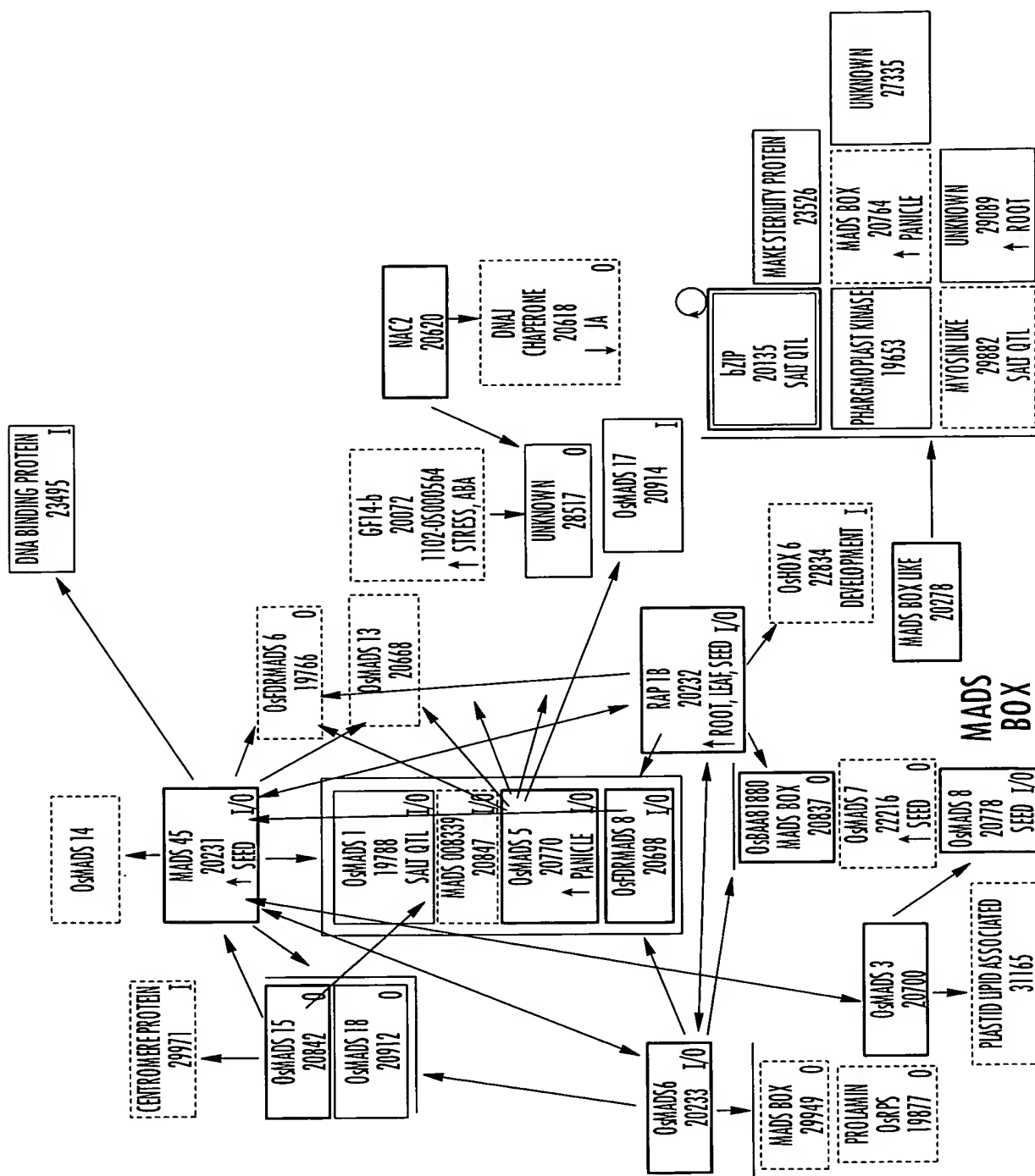
FIG. 1B3

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CELL CYCLE  
 FIG. 1C

**FIG. 2**





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CONS.	-----MGRGRVELKRIENKINRQVTGSKRRNGLLKKAYELSVLCDAEVALIIFSSRGKLYEFASSS	10	20	30	40	50	60	70
19766	-----MGRGKVQLKRIENTINRQVTFSKRRSGLLKKANEISVLCDAEVALIIFSTKGKLYKYATDS							
19788	-----MGRGKVELKRIENKISRQVTFAKRRNGLLKKAYELSLCDAEVALIIFSGRGLFEFSSSS							
20231	-----MGRGRVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSNRGKLYEFCSTQ							
20232	-----MGRGKVQLKRIENKINRQVTFSKRRSGLLKKANEISVLCDAEVALIIFSTKGKLYEYATDS							
20233	-----MGRGRVELKRIENKINRQVTFSKRRNGLLKKAYELSVLCDAEVALIIFSSRGKLYEFGSAG							
20278	-----MGRGKIEIKRIENATNRQVTYSKRRRTGIMKKARELTVLCDAQVAIIMFSSSTGKYHEFCSPS							
20668	-----MGRGRIEIKRIENTTSRQVTFCKRRNGLLKKAYELSVLCDAEVALIIVFSSRGRLYEYSNNN							
20698	MV-----RGRTELKRIENPTSRQVTFSKRRNGLLKKAFELSVLCDAEVALIIVFSPRGRLYEFASAP							
20700	-----MGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALIIVFSSRGRLYEYANNS							
20770	-----MGRGKVELKRIENKISRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSTRGRLFEFSTSS							
20778	-----MGRGRVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSNRGKLYEFCSGQ							
20837	MA-----RERREIKRIESAAARQVTFSKRRRGLFKKAEELSVLCDAEVALIIVFSSSTGKLSHFAS-S							
20842	-----MGRGKVQLKRIENKINRQVTFSKRRNGLLKKAEISVLCDAEVAIVFSPKGKLYEYATDS							
20847	EGEG--RAATGKRERIAIRRIDNLAARQVTFSKRRRGLFKKAEELSILCDAEVLVFSATGKLFQFAS-T							
20910	-----MGRGKVQLKRIENKINRQVTFSKRRSKLLKKANEISVLCDAEVALIIFSTKGKLYEYATDS							
20912	-----MGRGPVQLRRIENKINRQVTFSKRRNGLLKKAEISVLCDAEVALIIVFSTKGKLYEFSSHs							
20914	-----MGRGRVELKRIENKINRQVTFSKRRNGLLKKAYELSVLCDAEVALIIFSSRGKLYEFGSAG							
21116	LVGGSWRSIGMGRGRVELKRIENKINRKVTFAKRRNGLLKKAYELSVLCDAEVALIIFSNRGKLYEFCSTQ							
29949	-----MGRGKIVIRRIDNSTSRQVTFSKRRNGLLKKAKELSILCDAEVLVFSSTGXLYEFSST-							

FIG. 3A

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CONS.	S-MTKTLERYQRYSYA--ESAVISAESQTQGSWYQYLYKLKAKVEALQKTQRH-----LLGEDLESLSLKELQ	80	90	100	110	120	130	140
19766	C-MDKILERYERYSYAEK--VLISAESDTQGNWCHEYRKLKAKVETIQKCQKH-----LMGEDLESNLNLKELQ							
19788	C-MYKTLERYRSCNYN---SQDAAAPENEI--NYQEYLYKLKTRVEFLQTTORN-----ILGEDLGPLSMKELE							
20231	S-MTKTLEKYQKCSYAGPETAQNRESEQLKASRNEYLYKLKARVENLQRTORN-----LLGEDLDSLGIKELE							
20232	C-MDKILERYERYSYA--EKVLISAESDTQGNWCHEYRKLKAKVETIQKCQKH-----LMGEDLESNLNLKELQ							
20233	G-ITKTLERYQHCCYNAQDSNNALS--ET-QSWYHEMSKCLKAKFEALQRTQRH-----LLGEDLGPLSVKELQ							
20278	DIKGIFDRYQ-----QAIGTSLWIEQYENMQRTLSHLKDIRNRLRTEIRQRMGEDLDGLEFDELRL							
20668	N-VKATIDRYKKAHACGSTGAPLIEVNAQYQYESAKLRHQIQMLQNTNKH-----LVGDNVSNLSLKELK							
20698	S-LQKTIDRYKAYTKDHVNNKTIQDDIQQVK---DDTLGLAKKLEALDESRRK-----ILGENLEGCSIEELR							
20700	--VKSTVERYKKANS-DTSNSGTVAEVNAQHY-QQESSKLQQISSLQANANSR-----TIVGDSINTMSLRDLK							
20770	C-MYKTLERYRSCNYNLNSCEASAALETEL-SNYQEYLYKLKTRVEFLQTTORN-----LLGEDLVPLSLKELE							
20778	S-MTRTLERYQKFSYGGPDTAIQNKENELVQSSRNEYLYKLKARVENLQRTORN-----LLGEDLGTLGIKELE							
20837	S-MNEIIDKYNTHSNLGAEPQLDLNLEHS--K-YAHLNEQLAEASLRRLQ-----MRGEELEGLSIDELQ							
20842	R-MDKILERYERYSYA--EKALISAESSEGNWCHEYRKLKAKIETIQKCQKH-----LMGEDHESNLNLKELQ							
20847	S-MEQIIDRYNSHKTQRAEPSQLDLQGEDS--STCARLKEELAETSRLRLQ-----MRGEELHRLNVEQLQ							
20910	C-MDKILERYERYSYA--EKVLISAESDTQGNWCHEYRKLKAKVETIQKCQKH-----LMGEDLESNLNLKELQ							
20912	S-MEGILERYQRYSPD--ERAVLEPNTEDQENWGDEYGILKSKLDALQKSQRQ-----LLGEQLDTLTTKELQ							
20914	G-INKTLEKYNSCCYNAQGSNSALAGGEH-QSWYQEMSRLKTKLECLQRSQRH-----MLGEDLGPLSIKELQ							
21116	S-MTKTLEKYQKCSYAGPETAQNRESEQLKASRNEYLYKLKARVENLQRTORN-----LLGPDLDLSLGIKELE							
29949	N-MKTVIDRYTNAKEELLGGNAT---SEIKIWOREAASLRQQLH-NLQESHKQ-----LMGEELSGLGVRLDQ							

FIG. 3B

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CONS.	150	160	170	180	190	200	210
	QLEKQLESSLKHRSRKTQLLLEQISELQKKEKSLQEENKVLQKLVETEK---GQQVQQQG-WDQGQGQTP						
19766	QLEQQLENSLKHRSRKSQMLMESINELQKKEKSLQEENKVLQKELVEKQK----VQKQQ-VQWDQTPQT-						
19788	QLENQIEVSLKQIRSRKNQALLDQLFDLKSKEQQLQDLNKDLRKKLQETS-----AENVLHMSWQDGGGSHSGS						
20231	SLEKQLDSSLKHVRTTRTKHLVDQLTELQKKEQMVSEANRCLRRKLEESNHVR-GQQVWEQGCNLIYERQIP						
20232	QLEQQLENSLKHRSRKSQMLMESINELQKKEKSLQEENKVLQKELVEKQK----VQKQQQLQ-WDQTPQT-						
20233	QLEKQLECALSQARQKTKQMLMEQVEELRRKERQQLGEINRQLKHKLEVEGSTS-NYRAMQQASWAQAVVEN						
20278	GLEQNVDAAALKEVRHRKYHVTITQETTYKKVKHSYEAYETLQQLGLREEPAFGFVDNTGGGWDGGAGAGA						
20668	QLESRLKGIKIRARKNELLASEINYMAMKREIELQNDNMDLRTKIAEEEQQL-QQVTVARSAAAMELQAAAA						
20698	GLEMKLEKSLHNIRLKKTELLERQIAKLKEKERTL-----LKDNENLR-GKHRNLEAAALVANHMTT						
20700	QVENRLEKGIKIRARKNELLYAEVEYMQREVELQNDNMVYLRKVVENERGQ-QPLNM-----MGAASTSE						
20770	QLENQIEISLMNIRSSKNQQLDQVFELKRKEQQLQDANKDLKRKIQETS-----GENMLHISCQDVGPSG--						
20778	QLEKQLDSSLRHIRSTRTQHMLDQLTDLQRRQMLCEANKCLRRKLEESNQLH-GQ-VWEHGATLLGYERQS						
20837	QLEKNLEAGLHRVMLTKDQQFMEQISELQKSSQLAEENMQLRNQV-----SQ						
20842	QLEQQLESSLKHIISRKSHLMLESISELQKKEKSLQEENKALQKELVERQKNV-RGQQQVQG-WDQTPQVQAQ						
20847	ELEKSLESLGSLVKTSSKKILDEIDGLERKRMQLIEENLRLEQV-----SR						
20910	QLEQQLENSLKHRSRKSQMLMESINELQKKEKSLQEENKVLQKELVEKQK----VQKQQVQ-WDQTPQT-						
20912	QLEHQLEYSLKHRSKKNQQLLFESISELQKKEKSLKNQNNVLQK-LMETEKEK-NNAIINTN-REEQNGATP						
20914	QLEKQLEYSLSQARQKTKQIMMEQVDDLRRKERQQLGELNKLKKNLEAEADSS-NCRSAIQDSWVHGTVVSG						
21116	SLEKQLDSSLKHVRTTRTKHLVDQLTELQKKEQMVSEANRCLRRKLEESNHVR-GQQVWEQGCNLIYERQIP						
29949	GLENRLIEISLRNIRMRKDNLLKSEIEELHVKGSLIHQENIELSRSLNVMSSQK--LELYNKLQACEQATDAN						

FIG. 3C

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CONS.	--A-QQ-PPHSSS-F-HREAA--EPTLNIGY---AAGERIA-----Q-----LPP-WML-----	220	230	240	250	260	270	280	290
19766	-----SSSSSSFFMMREA---LPTTNISNYPAAAGERIEDVAAGQPQ-----HVRIG-LPP--WMLSHING								
19788	STVLADQP-HHHQGLLHPHPDQGDHSLQIGYHHPHAHHQAYMDHLSNEAADMVAAHPNEHIPSGWI-----								
20231	--EVQQ-PLHGGNGFFHPLDAAAGEPTLQIGY---PAEHHEA-----MNSACMNTYMP-P-WLP-----								
20232	-----ISSSSFFMMREA---LPTTNISNYPAAAGERIEDVPAGQPQ-----HVRIG-LPP--WMLSHING								
20233	GAAYVQPPPHSA-----AMDSEPTLQIGYPHQFVPAEAN-----TIORSTAPAGAENFM-LGWVL-----								
20278	AADMFAFRVPSQPNLHGMAYGGNHDRL-----								
20668	AQQQQQNPFVAAAQQLDMKCFPLNLFEEAAQVAVAAQRQQIIPTELNLGYHHHLAIPGATAADAPPPHF--								
20698	TTAPAAWPRDVPMTSSTAGAADAMDVEDTLYIGLPGTERSSNRSET-----								
20700	YDHMVNNPY-----DSRNFLQVNIMQQPHYA-----HQLOPTTLQLG-----QQPAFN-								
20770	-----NAS-EANQEFLLH--AICDPSLHIGY-----QAYMDHLNQ-----								
20778	PHAVQQVPPHGGNGFFHSLAAAEPTLQIGF---TPEQ-----MNSCVTAFMPT-WLP-----								
20837	ISPEA--KQVVDTENFVTEGQESVMTALHSGSSQSDNDGDGSDVSLKLG-----LPCGAWK-----								
20842	AQAQQAQTSSSSSMLRDQQALLPPQNICYPPVMMGERNDAAAAAQAQGVQLRIGGLPP--WMLSHLNA								
20847	MSRMEEMQPGDSEIVYEEGQESVTNASYP--RPPPDNDYSSDTSCLKG-----LHS-----								
20910	-----SSSSSSFFMMREA---LPTTNISNYPAAAGERIEDVAAGQPQ-----HERIG-LPP--WMLSHING								
20912	STSSPTPVTA DP-----IPTTNNSQSQPRGSEGEAQPSPAQAGNSK-----LPP--WMLRTSHT								
20914	GRVLNAQPP--P-----DIDCEPTLQIGY-YQFVRPEAA-----NPRSNGGGDQNNNFV-MGWPL-----								
21116	--EVQQ-PLHGGNGFFHPLDAAAGEPTLQIGY---PAEHHEA-----MNSACMNTYMPWLP								
29949	--ESSSTPYSFRIIQNANMPPSLELS-QSQQ--REGECSKTA-----APELGL-----HLP								

FIG. 3D

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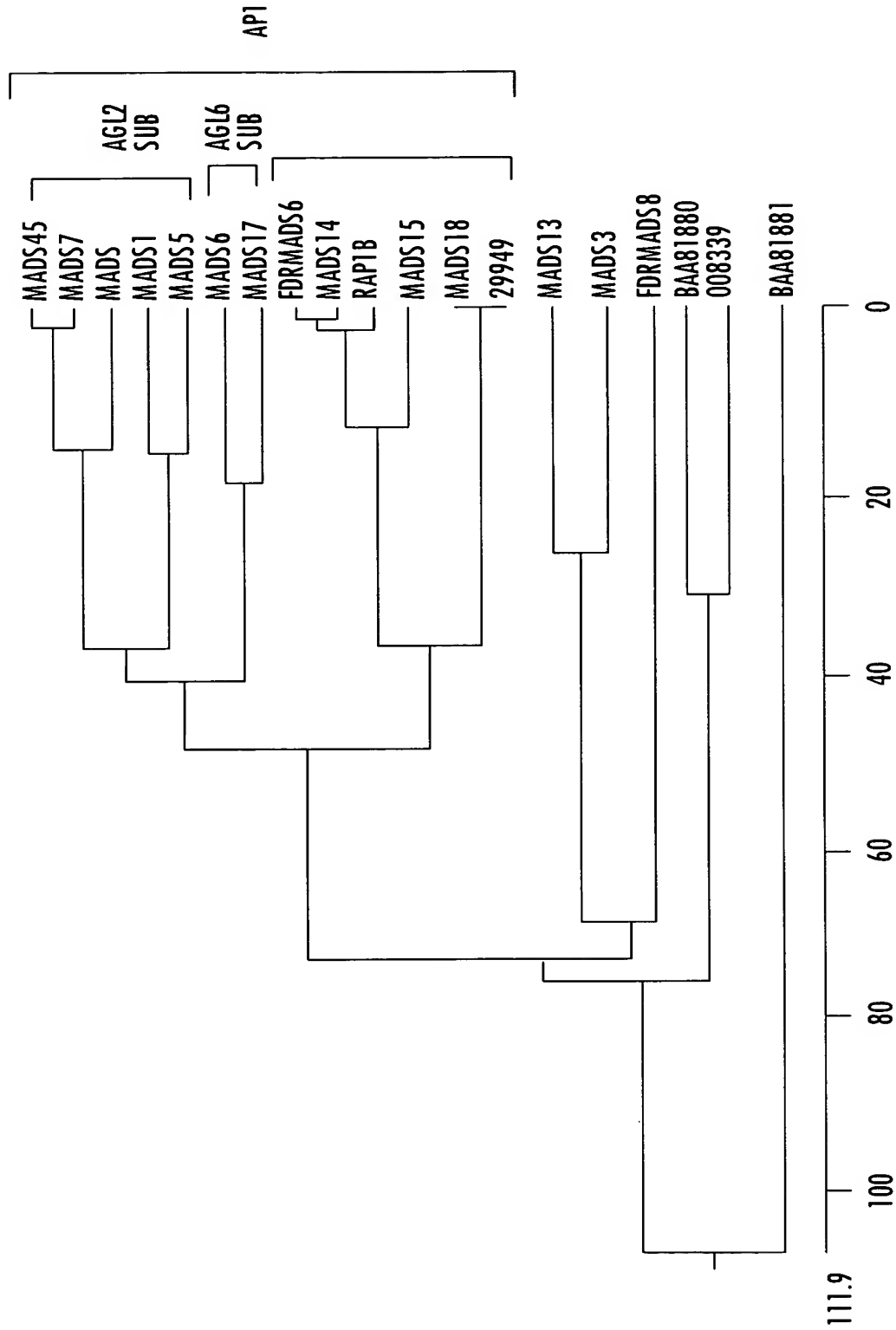


FIG. 3E

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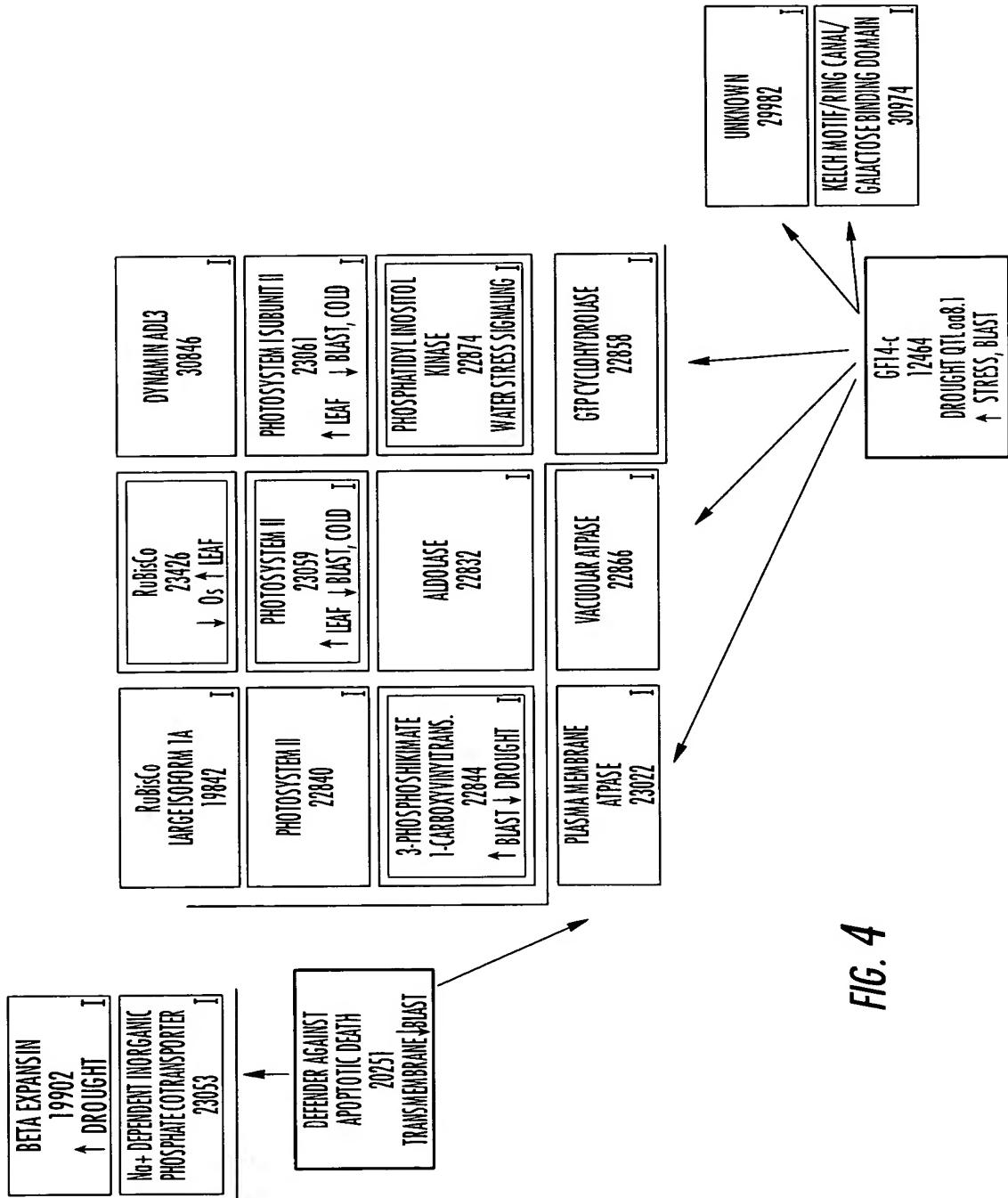
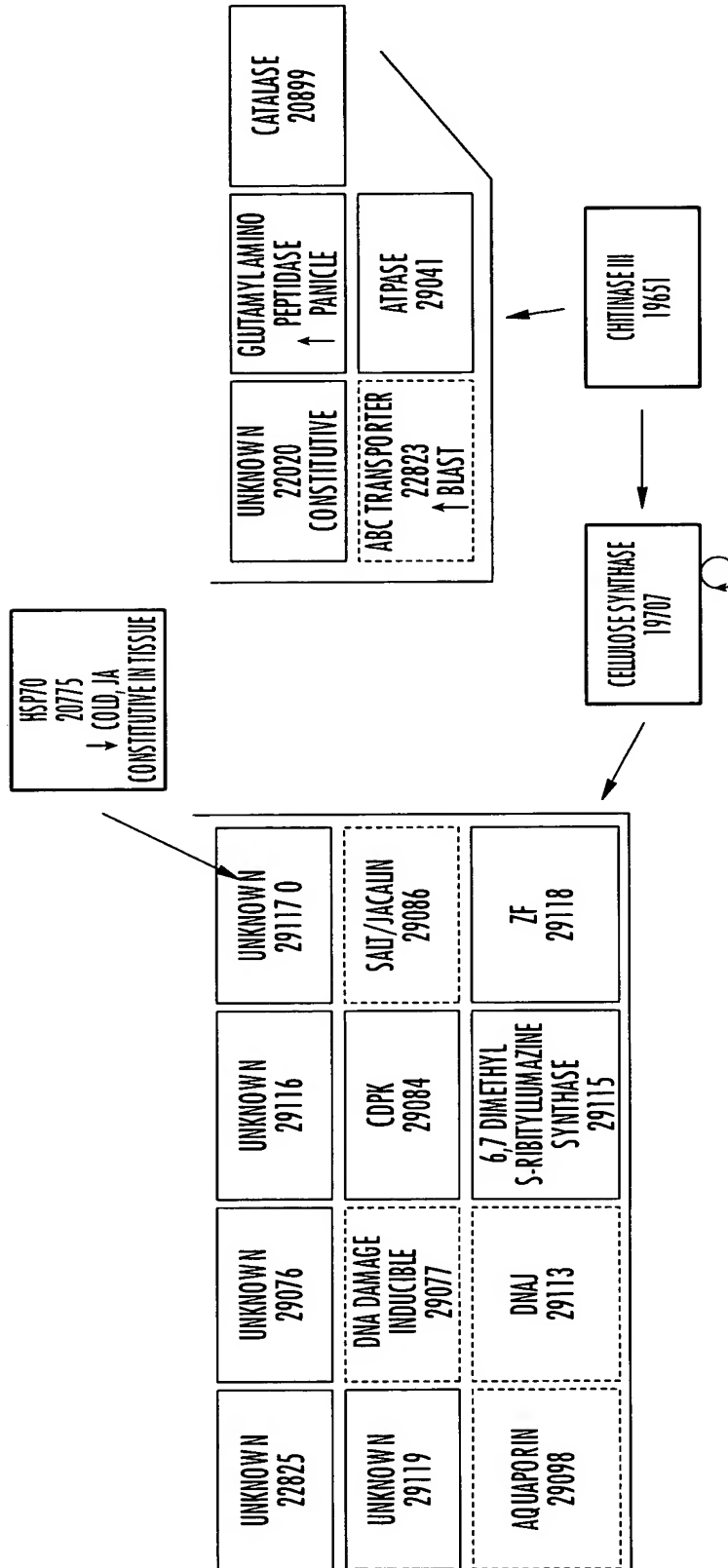


FIG. 4

## CHITINASE AND CELLULOSE SYNTHASE INTERACTIONS



**FIG. 5**

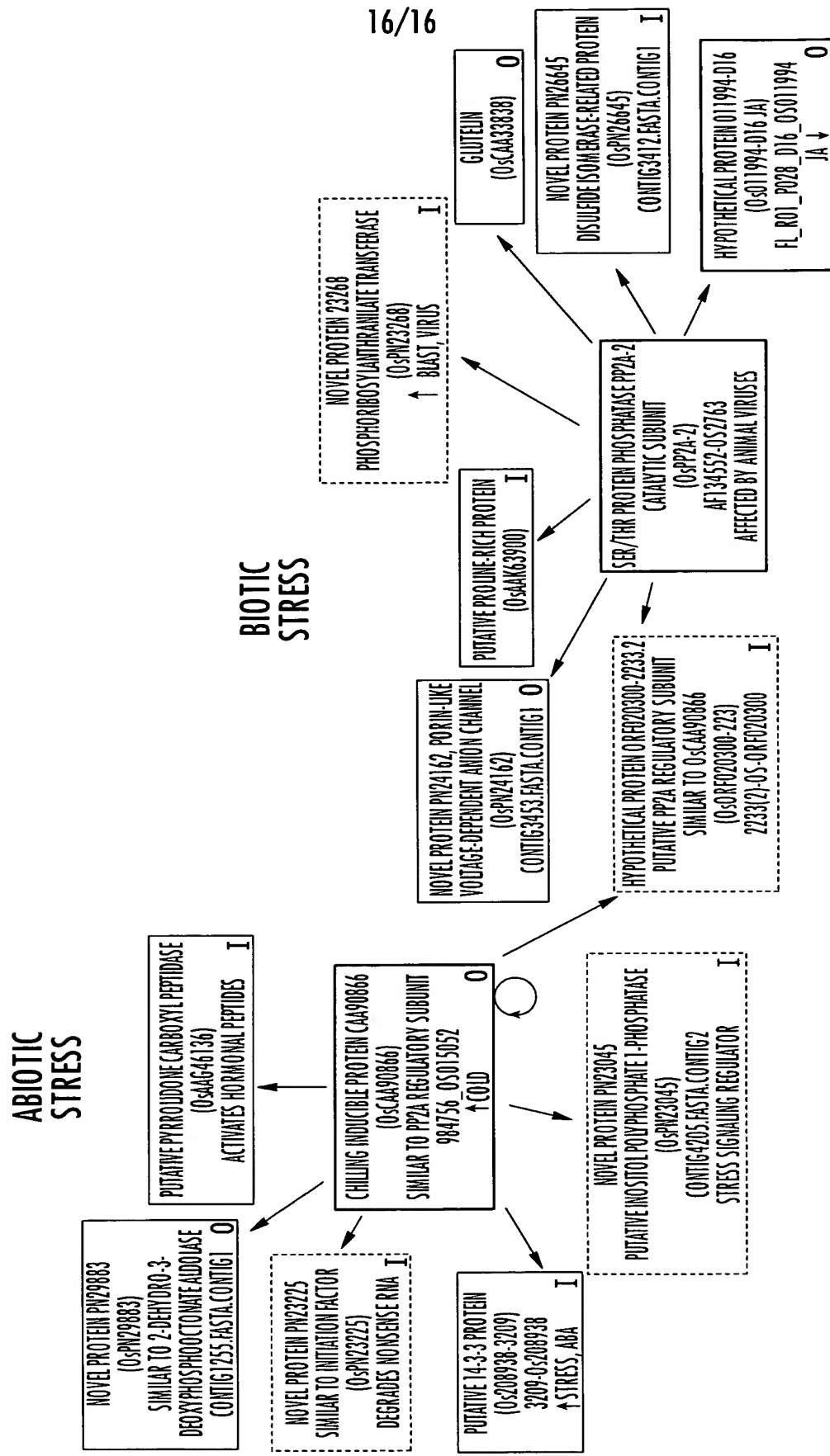


FIG. 6